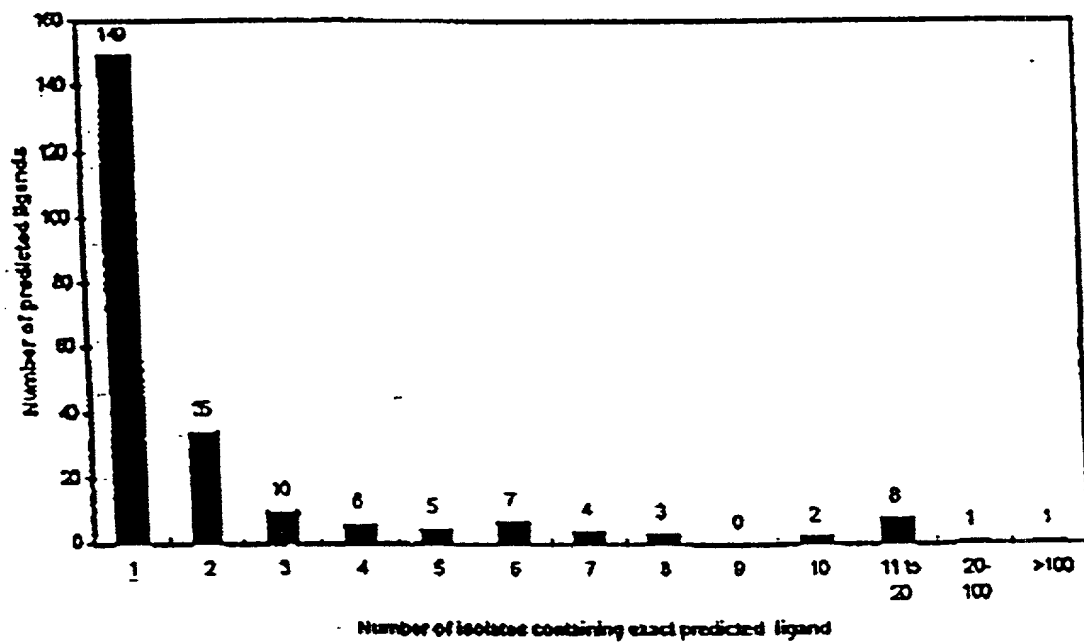


FIG. 1

a)



b)

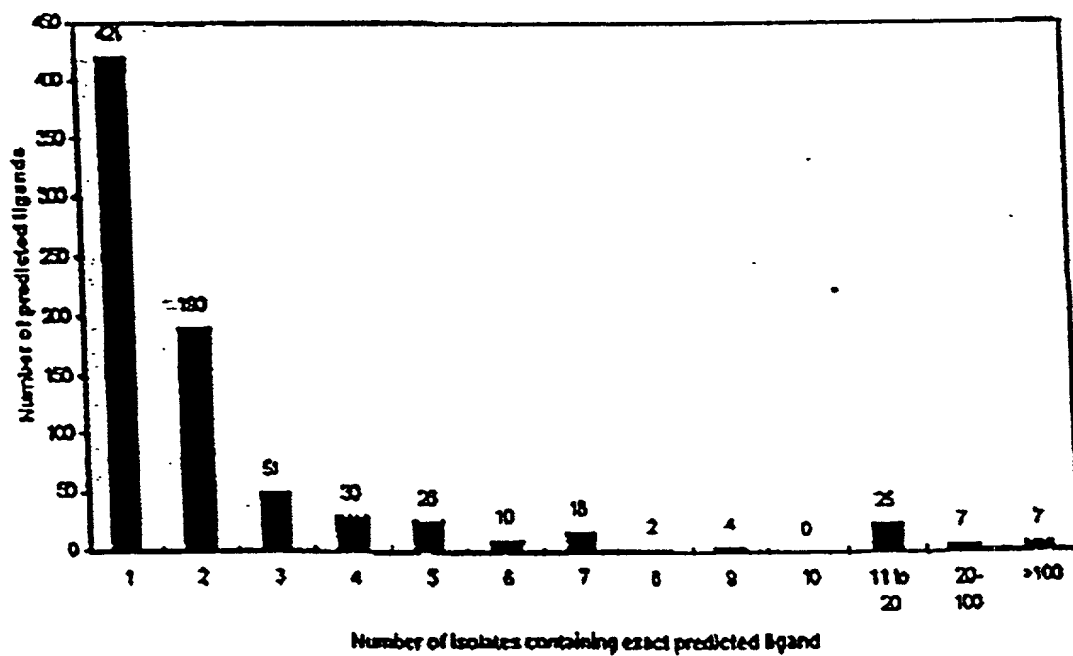


FIG. 2

Sequence	A2 EBP	B27 EBP	A2 Fold Increase (less than 1.3 not reported)	B27 Fold Increase (less than 1.3 not reported)	Protein	Number of Isolates with Exact AA	Approximate Position in LAI	Clade A	Clade B	Clade C	Clade D	Clade E	Other	SEQ ID NO.
KLTPLCVTLN	55.68%	0.00%	1.33		Env	159	gp120 - 120	X	X	X	X	X	X	1
AEWDRVHPV	66.42%	0.00%	1.35		Gag	36	gag - 215	X	X	X	X	X	X	2
SLFNTVATL	62.00%	0.00%			Gag	18	gag - 100	X	X	X	X	X	X	3
ELHPDKWTV	57.03%	0.00%			RT	17	RT - 354	X	X	X	X	X	X	4
GMDDPEREVL	72.52%	0.00%			Nef	17	nef - 170	X	X	X	X	X	X	5
GMDDPEKEVL	87.51%	0.01%	2.7		Nef	16	nef - 170	X	X	X	X	X	X	6
HLWRWGTMLL	76.69%	0.00%	1.33		Env	10	gp120 - 30	X	X	X	X	X	X	7
LLLTRDGGVN	55.68%	0.00%			Env	>10	gp120 - 452	X	X	X	X	X	X	8
HLWKWSTMLL	90.92%	0.00%	1.63		Env	>10	gp120 - 20	X	X	X	X	X	X	9
ILKEPVHGV	97.47%	0.00%	1.54		RT	>10	RT - 480	X	X	X	X	X	X	10
KRWILGLNK	0.00%	14.22%		3.61	Gag	79	gag - 263	X	X	X	X	X	X	11
CRUKQIN	0.00%	99.08%			Env	185	gp120 - 420	X	X	X	X	X	X	12
CRUKQINMW	0.00%	99.52%		1.74	Env	150	gp120 - 420	X	X	X	X	X	X	13
VSFEPIHF	0.20%	55.61%	1.45		Env	109	gp120 - 215	X	X	X	X	X	X	14
RCSSNTGL	0.01%	62.11%			Env	101	gp120 - 446	X	X	X	X	X	X	15
VSFEPIHY	0.00%	98.22%			Env	101	gp120 - 215	X	X	X	X	X	X	16
CRUKQIVNM	0.00%	91.33%			Env	75	gp120 - 420	X	X	X	X	X	X	17
IRSENIINN	0.00%	82.77%			Env	42	gp120 - 275	X	X	X	X	X	X	18
IRFIMIV	0.03%	89.06%			Env	19	gp41 - 175	X	X	X	X	X	X	19
ISFDPPIHY	0.01%	67.49%			Env	15	gp120 - 215	X	X	X	X	X	X	20
YRTGDIIG	0.00%	56.14%			Env	15	gp120 - 330	X	X	X	X	X	X	21
IRJPGQIFY	0.07%	75.36%			Env	13		X	X	X	X	X	X	22
GCSGKIIC	0.00%	61.09%			Env	12	gp41 - 90	X	X	X	X	X	X	23
RRRAPQDS	0.00%	67.49%			Tat	12		X	X	X	X	X	X	24
IRSENIITDN	0.00%	59.28%			Env	11	gp120 - 275	X	X	X	X	X	X	25
CRUKQFIN	0.00%	76.92%		1.53	Env	<10	gp120 - 420	X	X	X	X	X	X	26
KRISIGPGR	0.00%	56.93%		1.78	Env	<10	gp120 - 320	X	X	X	X	X	X	27
GQQIEQL	0.10%	78.93%			Env	<10		X	X	X	X	X	X	28
GRRGWELKY	0.01%	59.80%		3.27	Env	<10	gp41 - 270	X	X	X	X	X	X	29

FIG. 3

Project Outline

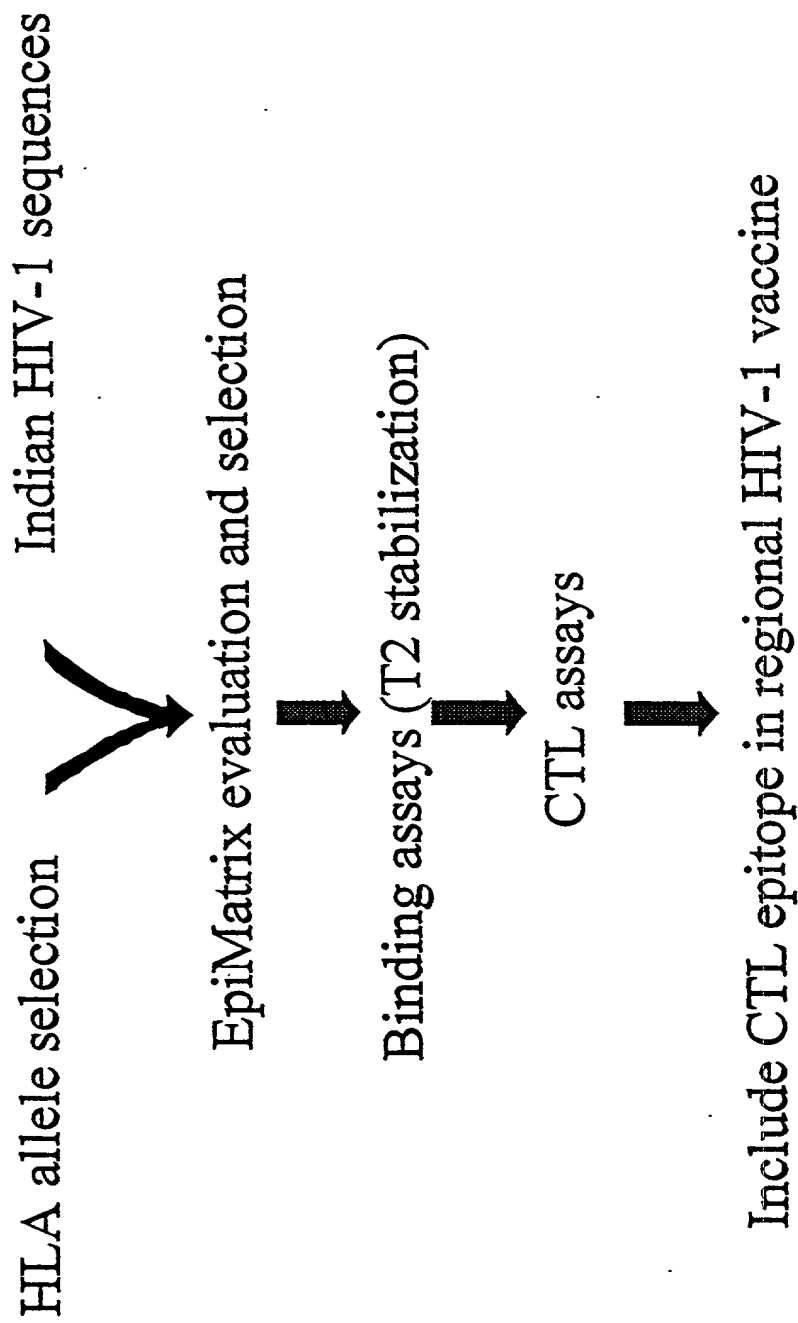
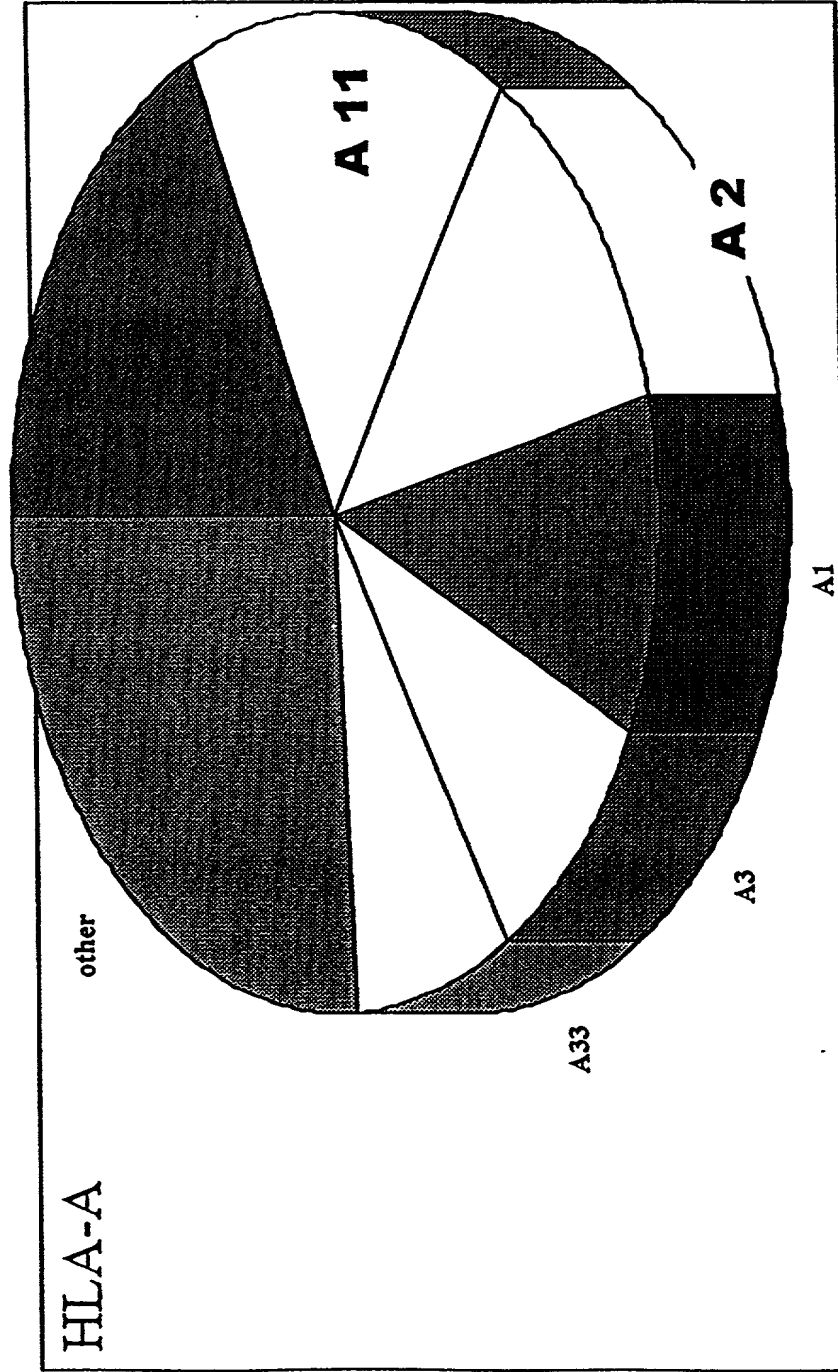


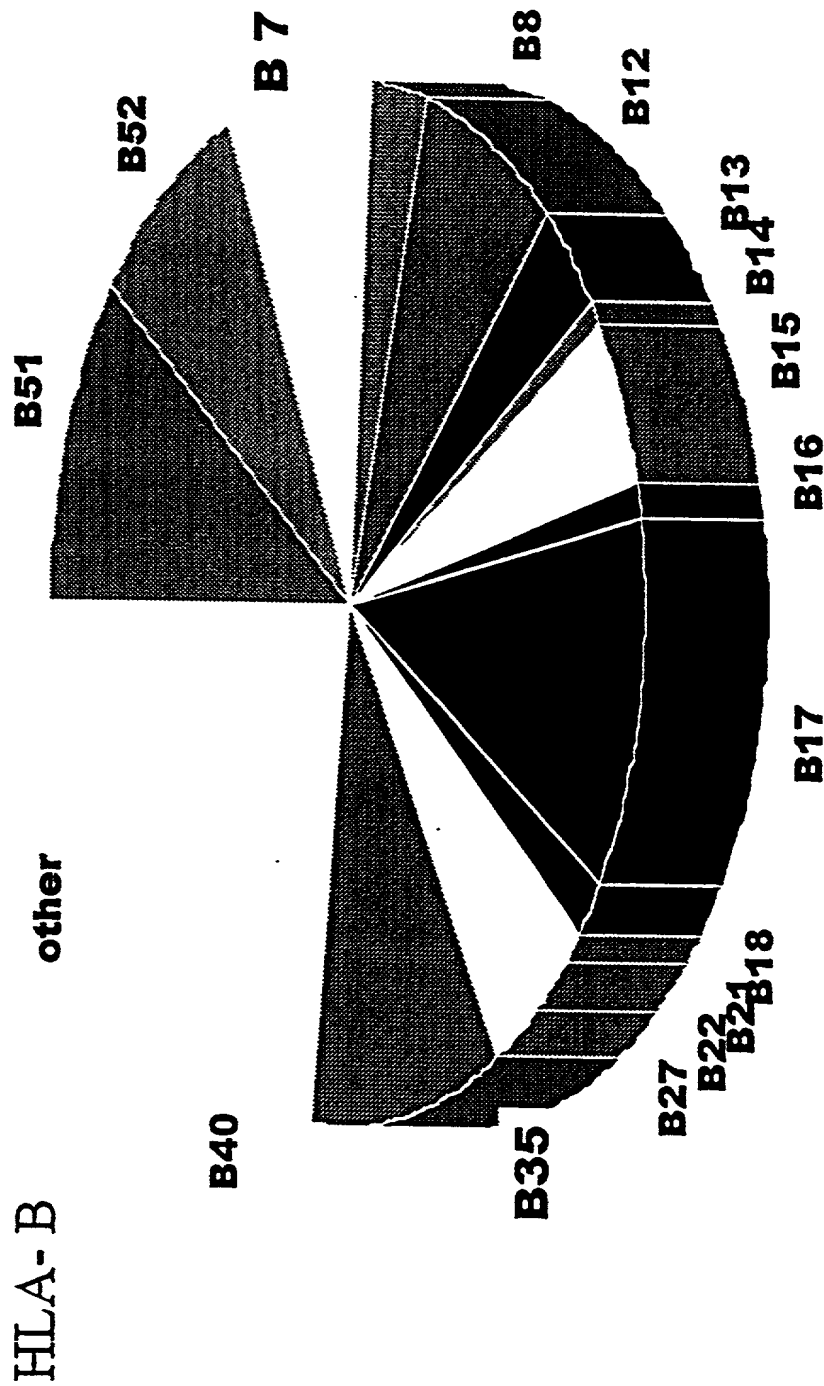
FIG. 4

Methods: HLA allele selection



HLA-A2 and -A11, -B7 and -B35 were selected for this pilot project due their prevalence of the HLA alleles in the Indian population....

FIG. 5
Methods: HLA allele selection



... and availability of cell lines for *in vitro* study.

FIG. 6

B7										
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBF	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
1	RPNNNTRKSI	RPNNNTRKSI	ENV	DID757	183-192	75	Y	8%	335.6	2.4
3	NPYNTPIFAL	NPYNTPIFAL	POL	Solnd5	61-70	60		20%	281.9	2.0
4	RAIEAQQHLL	RAIEAQQHLL	ENV	DID747	481-490	60		17%	181.5	1.3
5	TCKSNITGLL	TCKSNITGLL	ENV	DID760	375-384	59		18%	180.5	1.2
	KPWSTQLL	KPWSTQLL	ENV	DID747	182-191	71		48%	248.5	1.8
	KPCVKLTPLC	KPCVKLTPLC	ENV	DID747	51-60	100		27%	373.8	2.7
	GPVKQWPL	GPVKQWPLT	POL	Solnd4	25-34	100		27%	314.7	2.3
	YPGIKVRQL	YPGIKVRQLC	POL	Solnd4	278-287	100		28%	378.4	2.7

FIG. 7
EpiMatrix Predictions and Binding Results: B 35
7 out of 7 ... and control peptide

B37										
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBP	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
2	TVLDVGDAYF	TVLDVGDAYF	POL	SoInd4	114-123	100	Y	4%	47.9	1.6
6	EPPFLWMGY	EPPFLWMGYE	POL	SoInd4	231-239	100		9%	48.7	1.6
7	VPVKLKPGM	VPVKLKPGMD	POL	SoInd4	15-24	100		9%	53.3	1.7
8	CPKVTFDPI	CPKVTFDPIP	ENV	DID760	144-153	53		7%	35.0	1.2
	KPWVSTQLL	KPWVSTQLL	ENV	DID747	182-191	71		9%	40.5	1.4
	KPCVKLTPL	KPCVKLTPLC	ENV	DID747	51-80	100		11%	52.1	1.7
	GPKVKQWPL	GPKVKQWPLT	POL	SoInd4	25-34	100		11%	41.2	1.4
	YPGIKVRQL	YPGIKVRQLC	POL	SoInd4	278-287	100		7%	40.7	1.3

FIG. 8

EpiMatrix Predictions and Binding Results: A 2
3 out of 7 ... and control peptide

A2										
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBF	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
13	ILKEPVHGV	ILKEPVHGVY	POL	SoInd4	318-325	80	Y	96%	1804.2	1.6
14	QLPEKDSWTV	QLPEKDSWTV	POL	SoInd4	252-261	100		87%	1368.1	1.4
15	NLWTVYYGV	NLWTVYYGV	ENV	GrD1024	32-41	67		84%	1716.9	1.8
16	QMHEDVISL	QMHEDVISLW	ENV	DID747	37-46	91		78%	1413.1	1.4
17	KIEELREHLL	KIEELREHLL	POL	SoInd5	208-217	60		79%	889.9	0.9
18	DMVNQMHEDV	DMVNQMHEDV	ENV	DID747	33-42	64		77%	731.1	0.4
19	GLKKKKS MTV	GLKKKKS MTV	POL	SoInd4	106-115	100		76%	1088.4	1.1
20	ELHPDKWTV	ELHPDKWTVQ	POL	SoInd4	240-249	80		72%	1048.1	1.0

FIG. 9

EpiMatrix Predictions and Binding Results: A 11 4 out of 7 ... and control peptide

A11										
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBH	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
21	IYQEPFKNLK	IYQEPFKNLK	POL	Solnd4	348-357	100	Y	7%	677.5	3.1
22	VTFDPIPIHY	VTFDPIPIHY	ENV	DID780	147-156	53		22%	190.0	0.9
23	TVQCTHGIK	TVQCTHGIKP	ENV	DID747	174-183	59		44%	733.4	3.3
24	NTPIFALKKK	NTPIFALKKK	POL	Solnd5	64-73	60		44%	187.8	0.9
25	LVDFRELNK	LVDFRELNKR	POL	Solnd4	81-90	100		47%	755.2	3.4
26	PGMDGPKVK	PGMDGPKVKQ	POL	Solnd4	21-30	100		52%	193.8	0.7
27	GIPHPAGLKK	GIPHPAGLKK	POL	Solnd4	100-109	100		62%	309.6	1.4
28	FTTPDKKHQK	FTTPDKKHQK	POL	Solnd4	221-330	100		63%	920.6	4.1

FIG. 10

Methods: T2 Binding Assay

Allele matched peptides stabilize MHC molecules on the surface of TAP deficient cells. The stabilized MHC-peptide complex is detected using Ab to the MHC and fluorescence labeled secondary Ab.

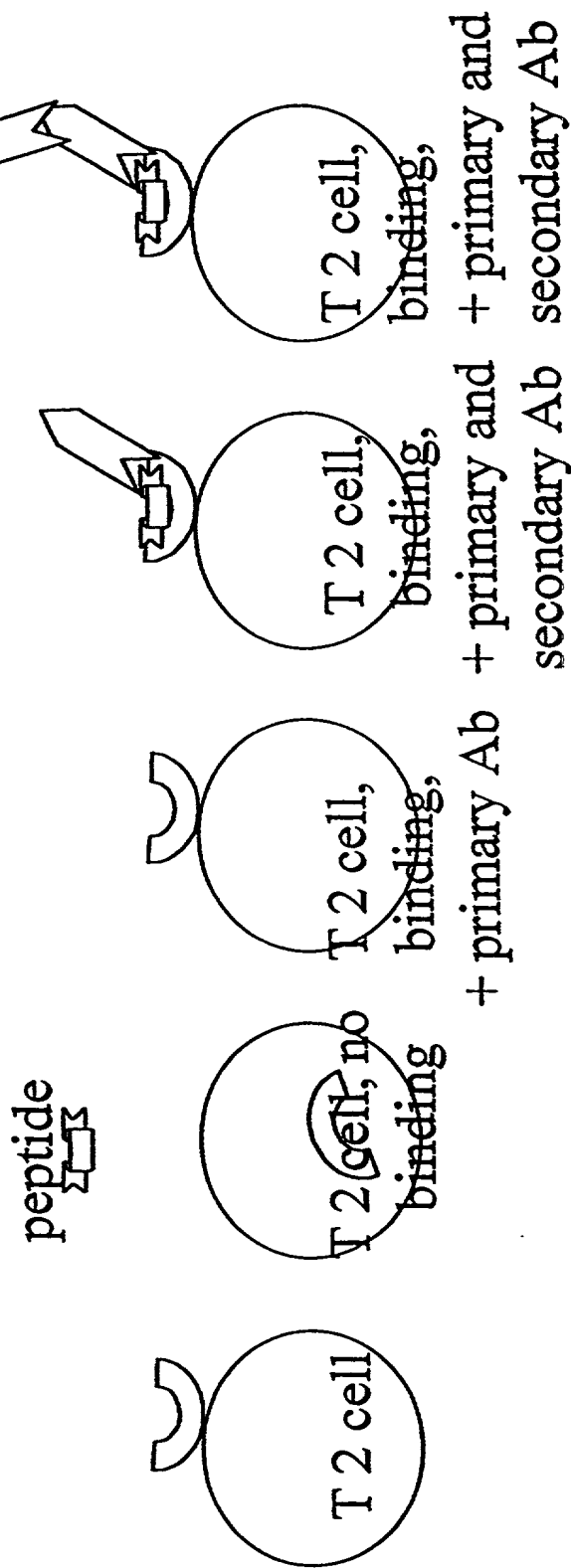


FIG. 11

Clustering of putative MHC ligands in *env*

